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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=18; hr=18; min=38; sec=30; ms=789;  
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Application No: 10590464 Version No: 1.0

**Input Set:**

**Output Set:**

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**Finished:** 2008-10-21 19:04:06.187  
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**Total Errors:** 0  
**No. of SeqIDs Defined:** 29  
**Actual SeqID Count:** 29

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**Input Set:**

**Output Set:**

**Started:** 2008-10-21 19:04:04.576  
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**Total Warnings:** 25  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 29  
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Error code	Error Description
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City of Yokohama

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structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

<140> 10590464

<141> 2008-10-21

<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
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35 40 45

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
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tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144  
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
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tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144  
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96			
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
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Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val			
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Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu  
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ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg 144  
Pro Gly Leu Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu  
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Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala  
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65 70 75 80

gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc 288  
Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr  
85 90 95

gtg tcc cga ttg ctg cgg gtt atg cag tgt ctg tcg cgg att gaa gaa 336  
Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu  
100 105 110

ggg gaa aat tta gac tgt tcc ttt gat atg gag gct gtc aca cca 384  
Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro  
115 120 125

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Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys			
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Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu			
245	250	255	
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Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro			
260	265	270	
gca agg cag cta cgg aat cct cca acc acc att gga atg atg act ctg			864
Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu			
275	280	285	
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370 375 380

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